

FIG. 1A

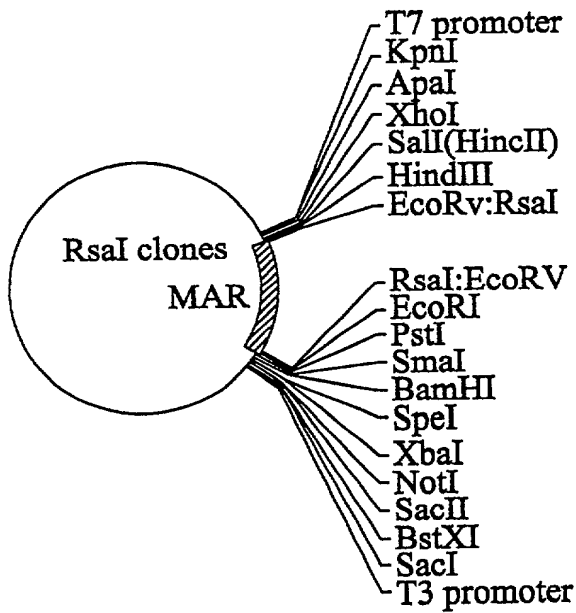


FIG. 1A.

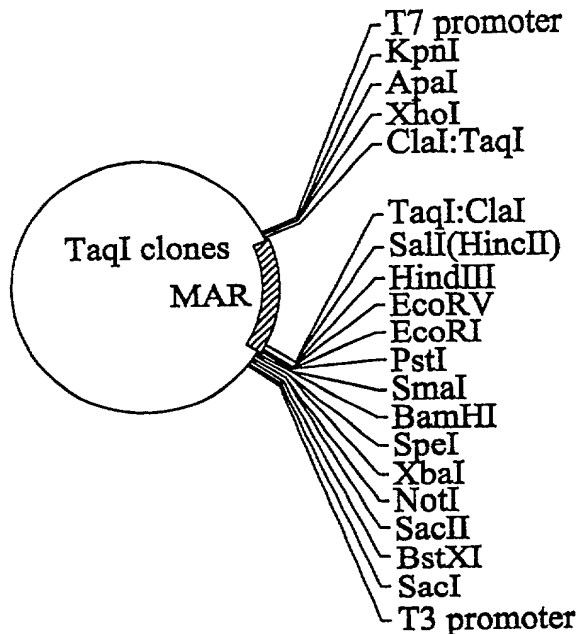


FIG. 1B.

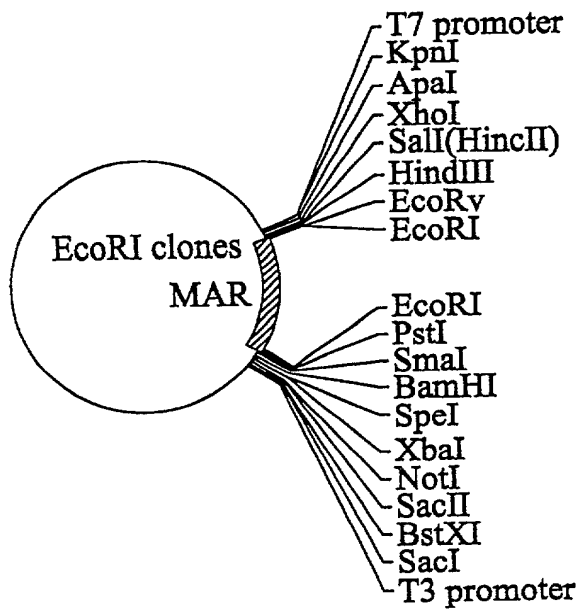


FIG. 1C.

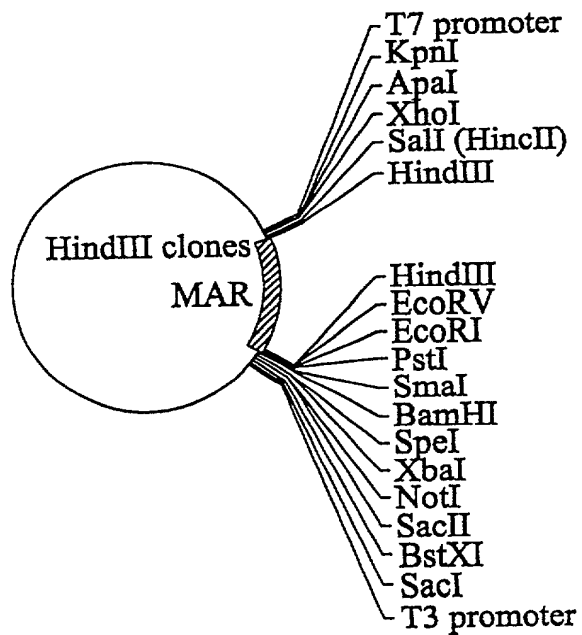


FIG. 1D.

FIG. 1E.

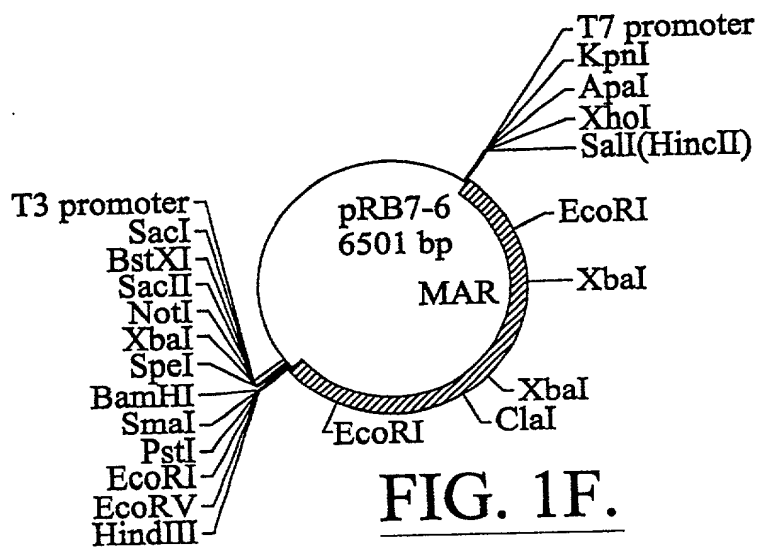
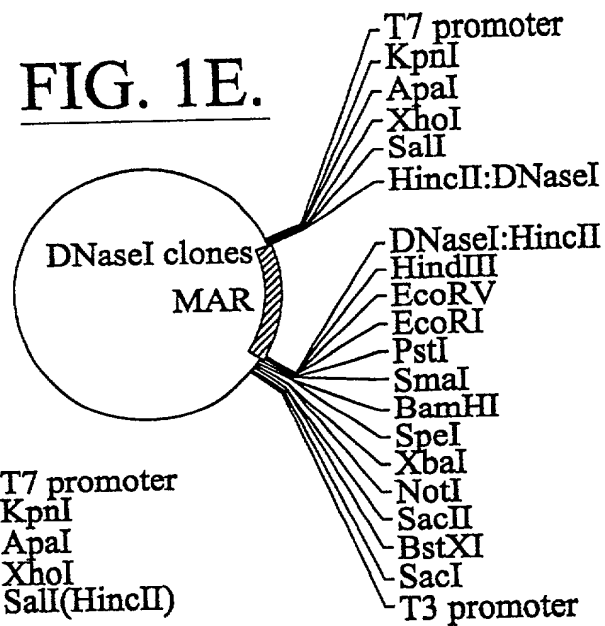


FIG. 1F.

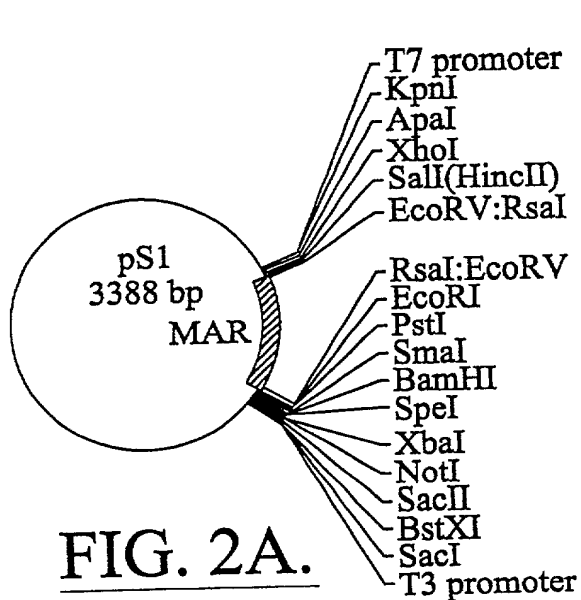


FIG. 2A.

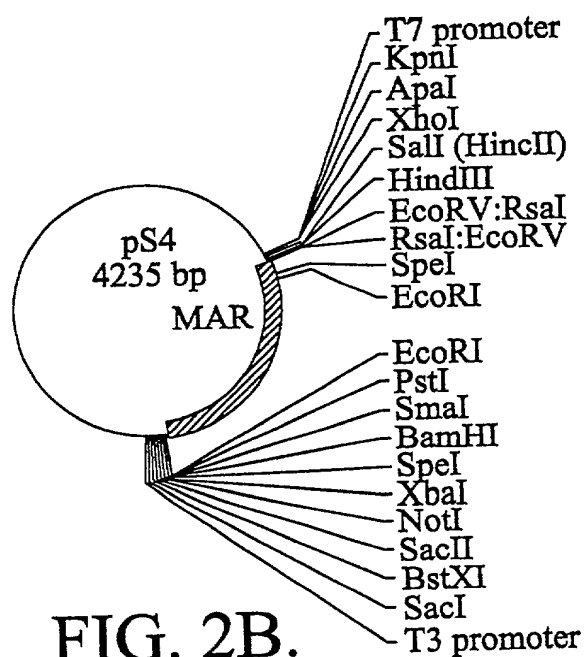


FIG. 2B.

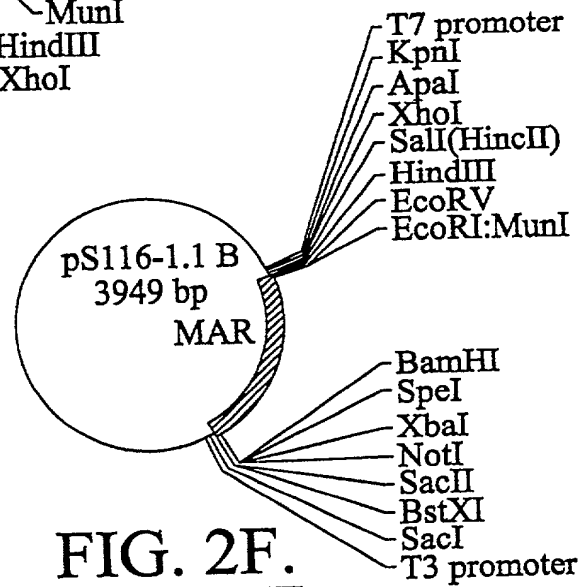
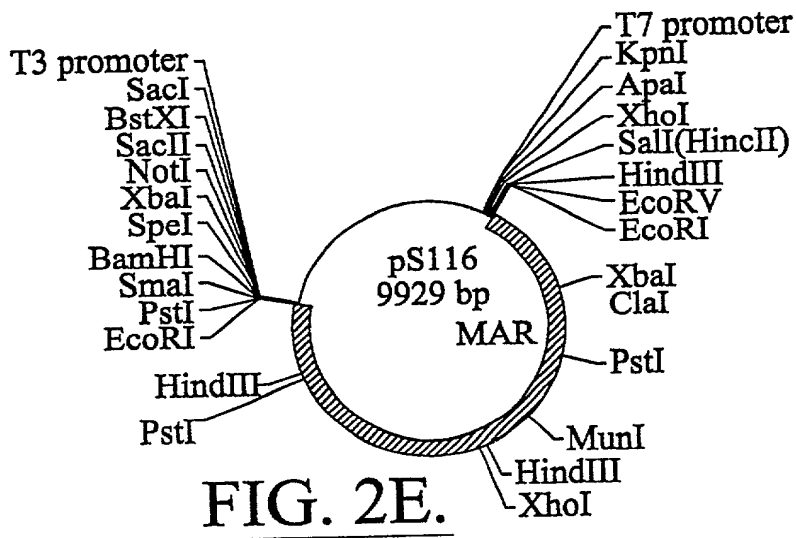
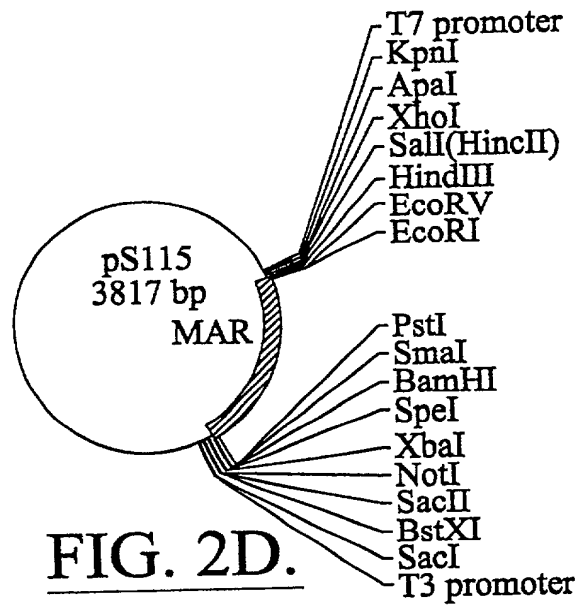
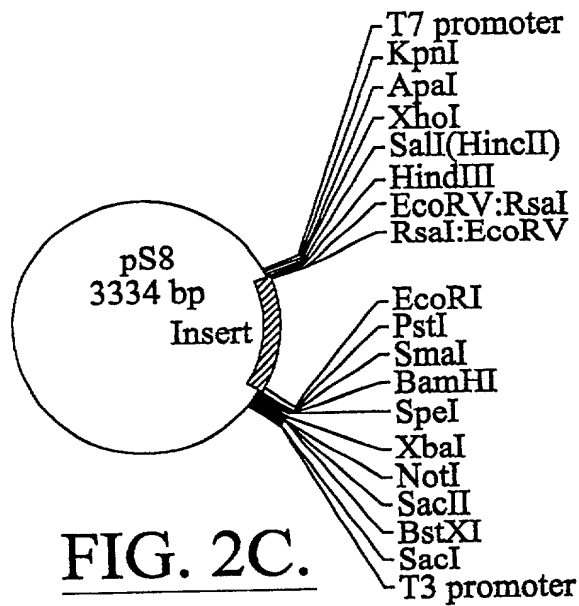


FIG. 2G.

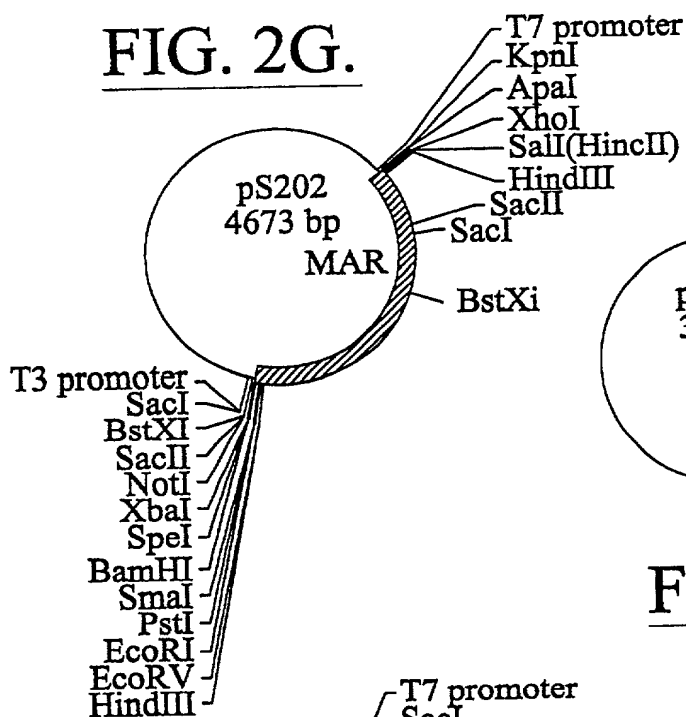


FIG. 2H.

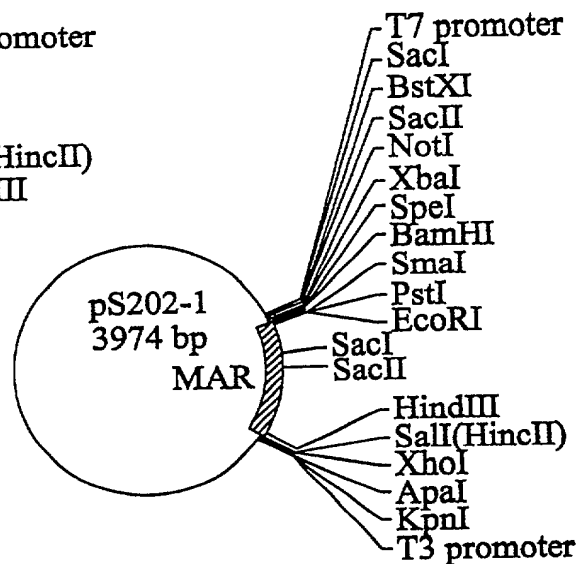


FIG. 2I.

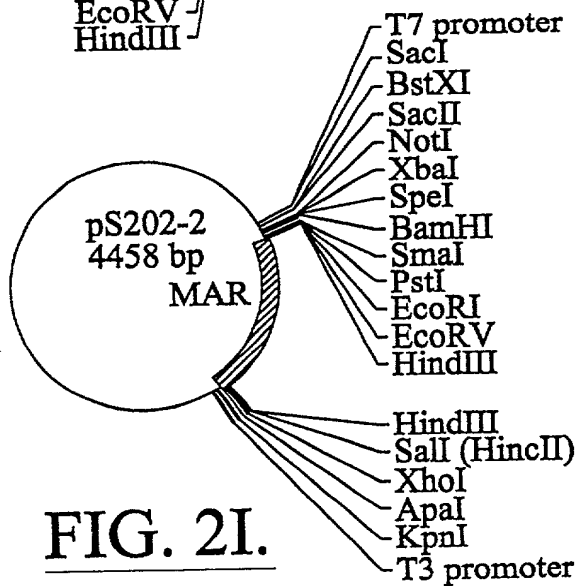


FIG. 2J.

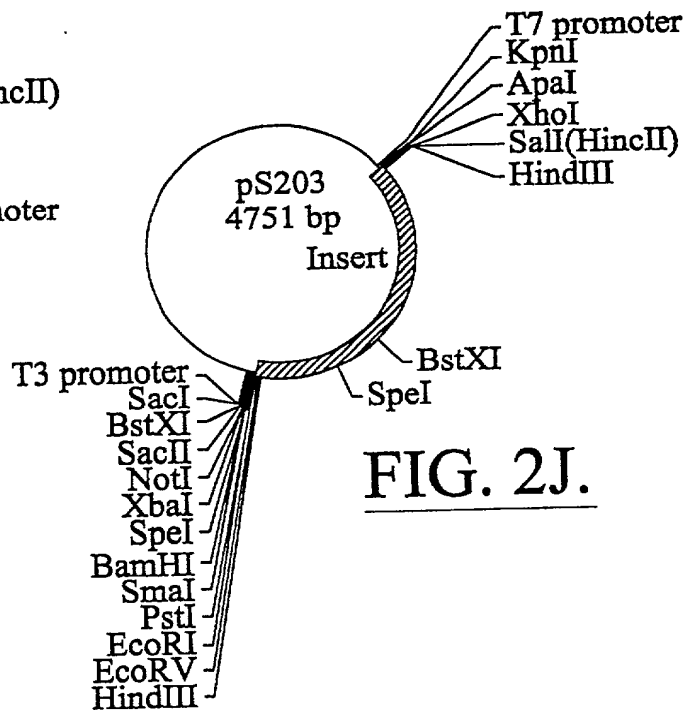


FIG. 2K.

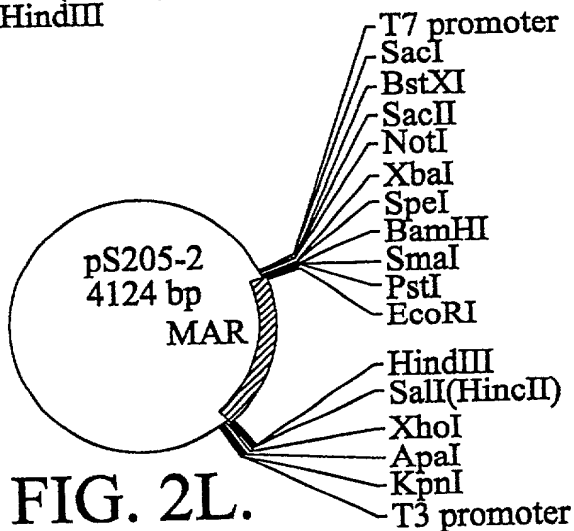
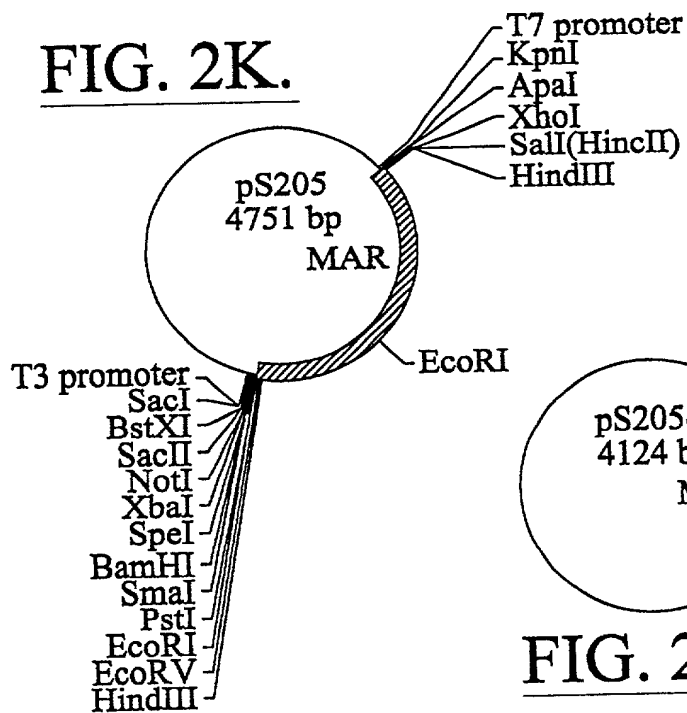


FIG. 2L.

FIG. 2M.

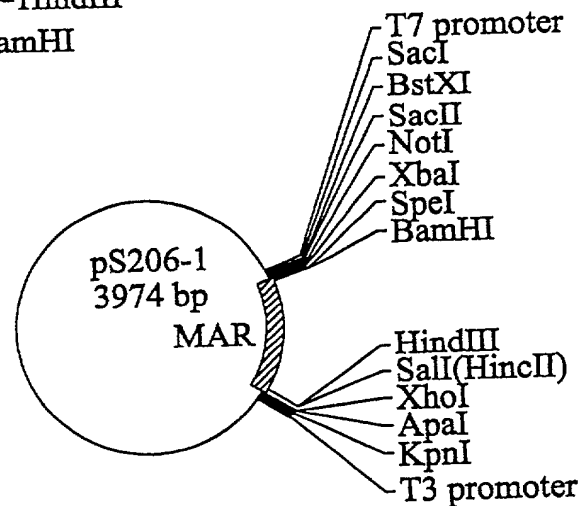
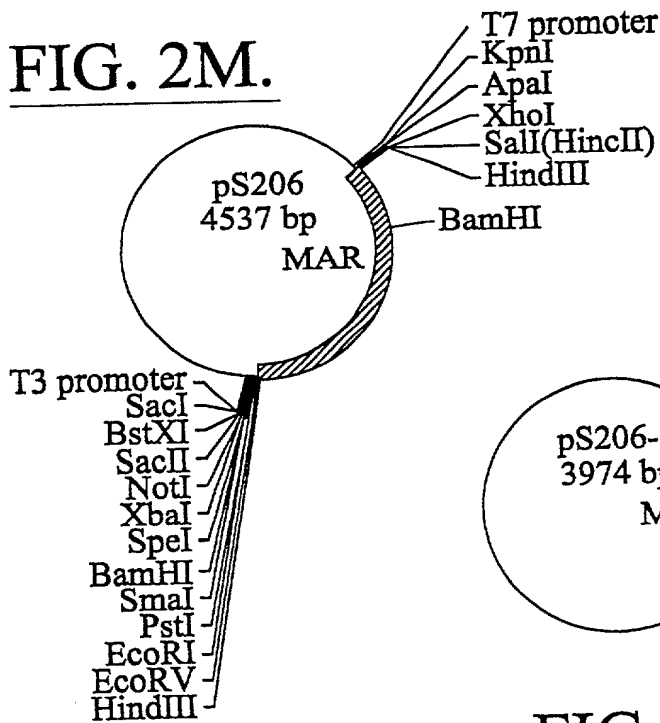


FIG. 2N.

FIG. 2O.

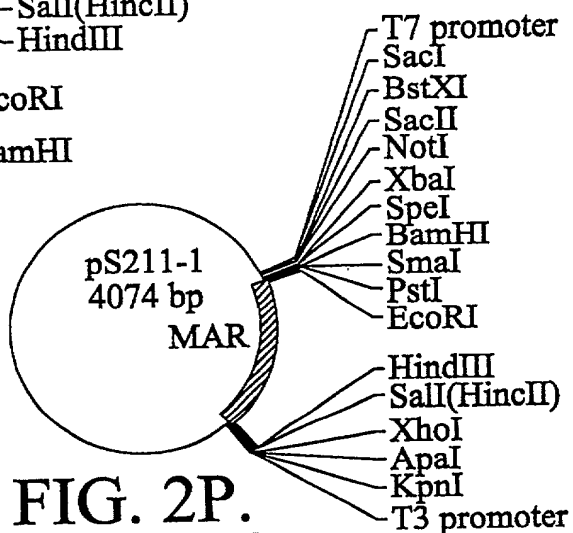
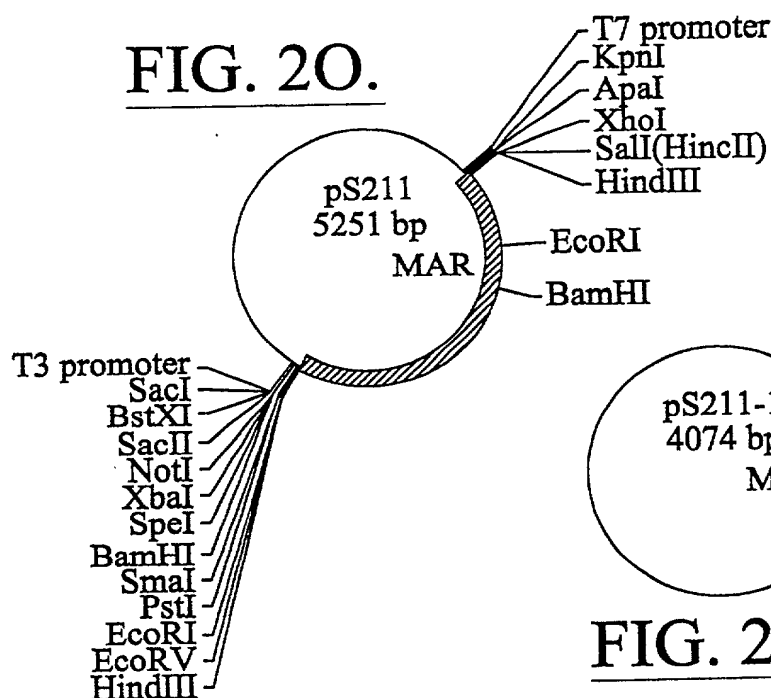


FIG. 2P.

FIG. 2Q.

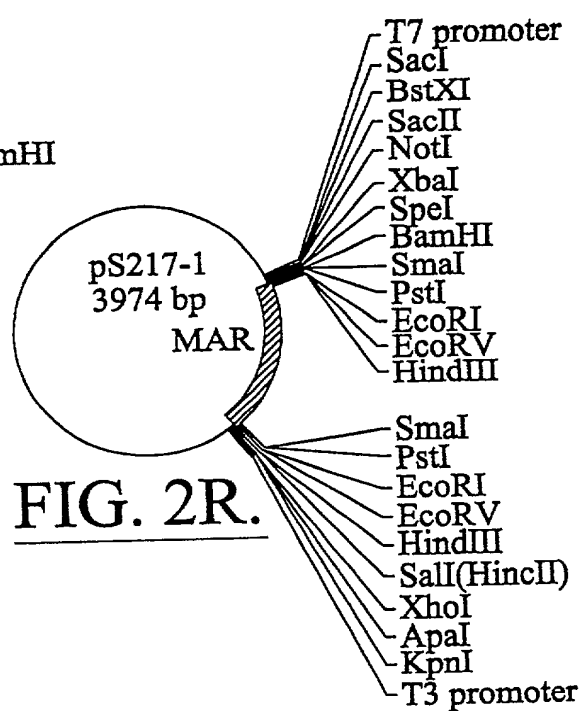
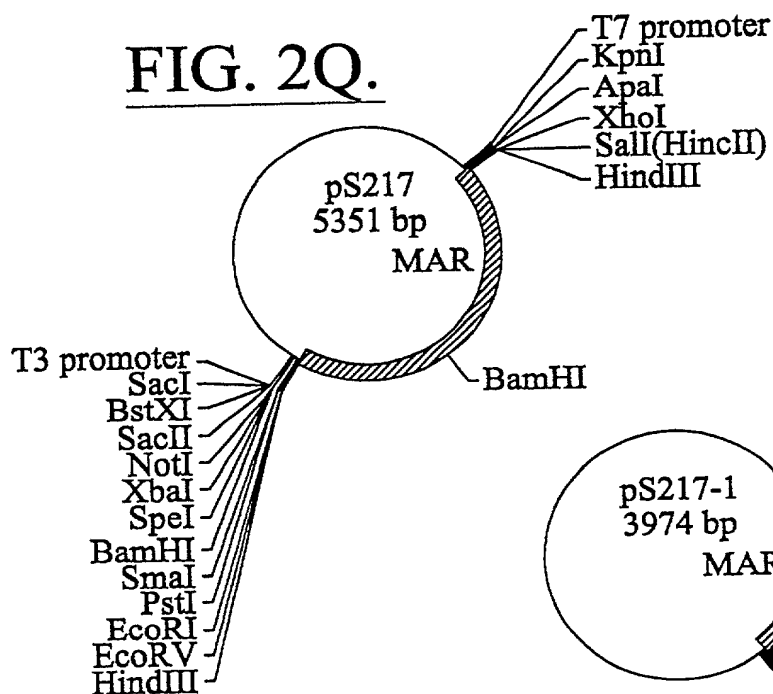


FIG. 2R.

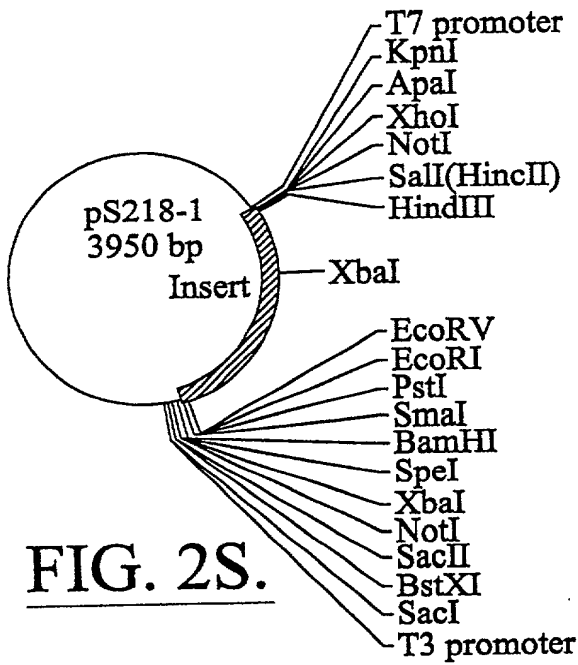


FIG. 2S.

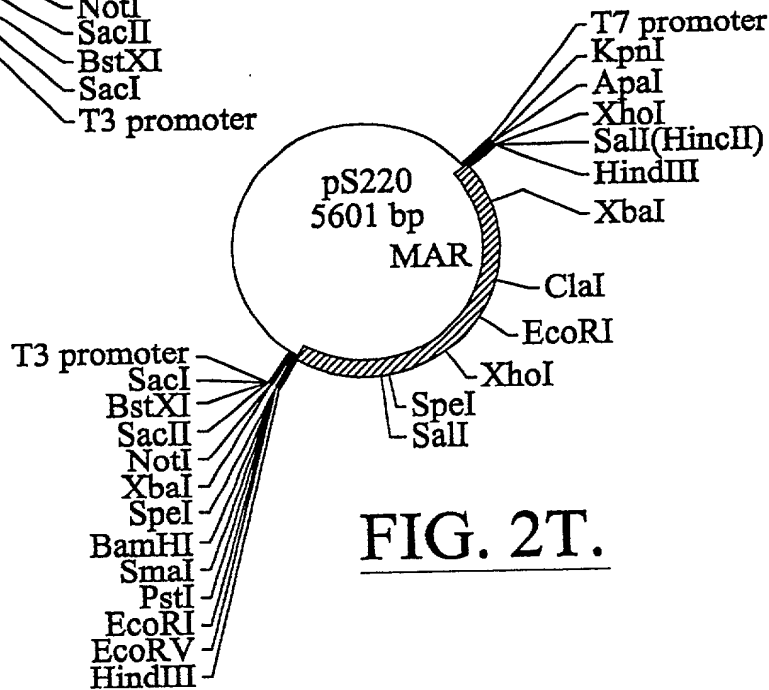


FIG. 2T.

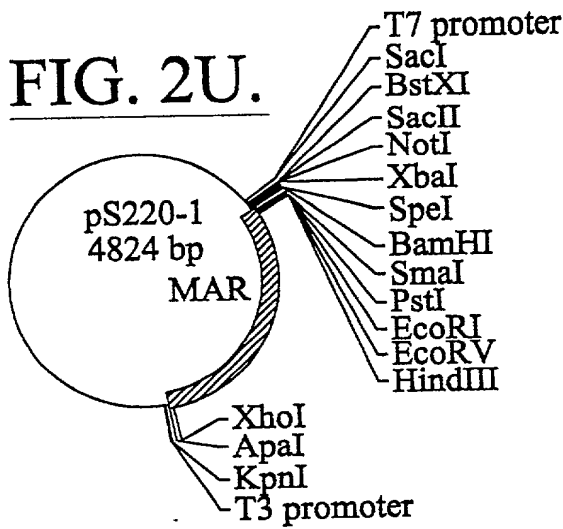
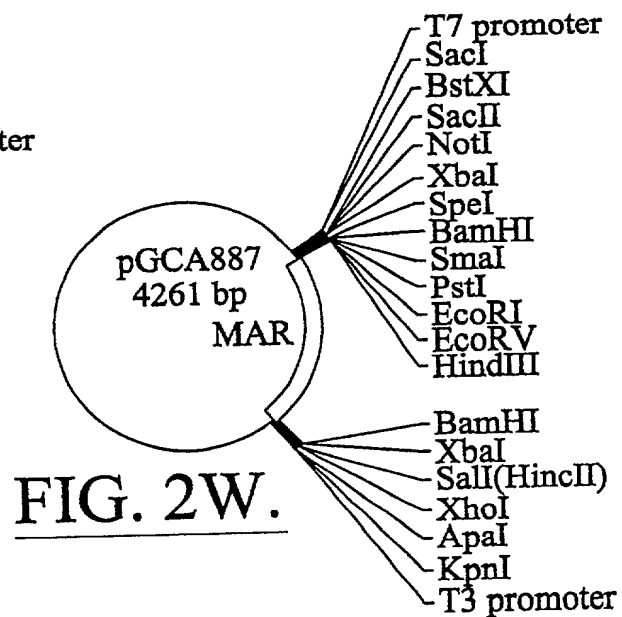
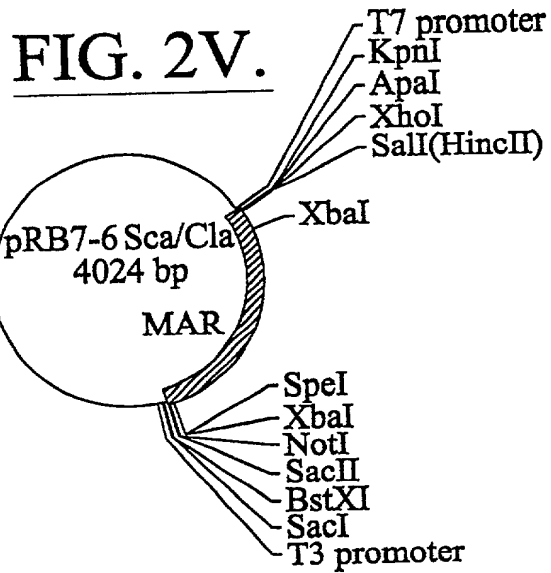


FIG. 2U.



pS1 (SEQ ID NO:1)

1 GATACGTAAA CAACGTGTAT CCAGTAAGTA TCAAGCCTAA TCTCGAAGTG
 51 GTAGAGACGA GATGACCGAC TTTGACACTC ACTATGGGTC AATAATAATA
 101 ACTGAAATAA AACTAAGATA TTTAAACCAA CATGATTTAC AGAATTTACA
 151 ATAATTTATT TAATCAGCAG AAATAATCAA ATTTCTTCAA ATGTAACAAT
 201 TCTCAATATA TTAATTAAAT TCCTTCAATT CAAATAATTT CTAATTTATC
 251 AATTAAACCT CATTTACAGG AGTAACAATT AATTCCTTAA CAAGCAAGAA
 301 TAATAATTCA TTAAATTCCA AGGATTTTTC AATTTATTAA TTAGCTTCAC
 351 AACCTGAAAT AAATTATTAA AGTATCGTGT AATTATTATT ATTAAGCACG
 401 ATTTCTGCCG AGGACATACG GCCCGATCCA GAGTATC

pS4 (SEQ ID NO:2)

1 GATACTAGAG TGGTGTATC AATTCTTACT CGTATGAATT AATTAAATTT
 51 GTCTCTTATT TCTGTCCTAA GTCATATACA AGAAATGCTA ACTCCATCCG
 101 TTTCAATCCC TATGACATAG TTTGATTTGA TTGAATTTGA AAATTTAAGA
 151 AACAAAAGAT AATTTTTGTG ACTCATAATT TAGACATGTG TTATAAGACT
 201 TTTCTCATGA ATTTTTTAGA AACAAATGAT AATTTTTGGA ACTCATAATT
 251 TAGACGTTTT ATAAAAATA CTAAGTGCAT CTGGTTCAAT ATTTATGTGT
 301 TATTCCTATA AAACCTCTGG ACTTATATTT TTAAATATTT CATAATATTT
 351 GGTATCGGTA TAATTTTTTT GTCACCTTTG GATGAAAGGG AAGTTTAAGT
 401 AAATTTCTTT TTCCAAATTT AGAAAGTTAT AATATTCTTT TTAAAACGCC
 451 CAAAAAGAAA AATAAGCTAT TGATTATTAT AAGCCTAAAC CAAAAGAATT
 501 CTTTGACTAG TAGGAAGCCA TTTTAAAGTT AGGCGCCAAA ATTCAAAGCC
 551 AACGTGGGCA TATCTCCAAA CTGGCGGCTA CAGTATC

pS8 (SEQ ID NO:3)

1 ACCGCTTTTA TTATTATTAT TTTTACCGAG AATTACAACA TCATGAAAAT
 51 ACATCTCGAA CCACGTCACA TCAATGCACC CGCGGTTATT GACATATTTT
 101 AACTCTGTTG AGATTTGGAT TTGGGTCACA TAAATGTGCA CCCGAGTTTA
 151 AGAGGATAAC ATTATTAAAT ACGCGCCTAA AACGACTAGC GTATCATTAT
 201 TTTGGGTAGG GCCGTGAAAT TTTGCTAAAC TGCCCATCCA GAAATCTAAG
 251 TAATTTTACC AACACGTATA GAGGGCCCCA CAGCTTGTGT ATTTTGTGTT
 301 GTCGAGGCTC GTCTCATTCA TTATTTTAA AAGGAATTG CAACGTCGTG
 351 GAAATGCATC TCGAACCACG TCACAATCAA TGA

FIG. 3.

pS115 (SEQ ID NO:4)

1 GAATTCGATA GACTCACTTA AATATTAGAA GTGAATTACC TAGAGTTAGA
51 TCCAAAACAA TTATCTTGCA CCTATCCTAT CAACCCCTAT CTTTTCCCAT
101 TGATTACTAC CTTGCTTACC TTTGTTACGA TTTTCATTAG ACAATAACTT
151 TAGATTCTTA GTTAATTGCA GTTAGAAATT ATATTAAATT TCAATTGTTG
201 GATCATCTTG AATACCAATC AAGCTAGAAA ATACAAGAAT ACTGTTTAAA
251 TCAAATCCAT GTGGATACGA TATTATACTA TATTATATTT GACTTGTGAG
301 CATTATTTAT GTGTGTTTTG TGCTCGTCAA AGTTTGGCGT CGTTGCCGAG
351 GATTGGCAAT CAATAGTGT TGAAATAGTT TTTGGTGCTA ATTTAGGAAT
401 TAGGTTTTAT TTATTTATTT TTTCTTTTCT TTTCTTTTTC CTTTCTATT
451 TTATTTCCCTT TATTAGTTAA CTTCTTTTCA AGATTTTTTT TGTAGTACCT
501 AACAAAGTTAG AGAAGATACT GTAGATTTTG AACTCTAAAT GTTGTGAAGA
551 TGGAGTACAA CCAGCCTAAG AAAATATTTG AATAGTTAGC AGCTGAACAT
601 TATCGGCGGT CGGTTATGCG GTTTAAATGC GGTGGAAGCA TCTACCACCG
651 CAGCCTAAAG AAAATATTTT GAATAGTTAG CAGCTTGAAC ATTATCGGCG
701 GTCGGTTATG TGTTTTAAAT GCGGTGGAAA TCATCTACGG GCTAACTGTC
751 AAGCAGGTAT GTATTCTTCC TATGGTTCGT ATTTTGAGGA GTCTCACTCT
801 GTTCTAGTT CGTACATGTA TGAGGATTCA TATGGGCACA ACTCTGACTC
851 TGGTTGGGAT GAATTC

pS116-1.1B (SEQ ID NO:5)

1 GAATTGTATT ATTGTTAGGT GGGAGAGATT TTTGACTATA TGGGTAAAAA
51 TCAGCGACAA AGGGCCAAAT ATACCTATTT ACTTTTAAAA ATAGTCTAAT
101 AATACCTCTC GTTATATTAT TAGGTTATCT ATACCTTTGC AGTCATATTT
151 TGGGTTCAAA TATACCCCTC ATTTAAACGG AGGGACACGT GTCATCGTCC
201 TGTTGGTCAA TTCTAAATAT CTCCTAATTA ATTA~~AAAA~~AGA CTCATTACCC
251 ATATCCGAAA AATATTTTTT AAAGCAATAT TTTTTTATAA AAAATGGAAA
301 AACTGAAATT ATTTTACTA AAAATTGAAA AAAACGAAAA TAGTTTTTTT
351 TCAGTTTTTA CAAAAAACT ATTTTAGAAA AAATTGAAAA ATATTTTCTA
401 AAACAATGTT TTTGTAAAAA CTGAAAAAAA AGAAGCTGAA AATCAATTTT
451 CTAAAGCAAT TTTATTTGTA AAATCTGGAA AAAACTACTA AAAACTGAAA
501 AAATGAAAAT ATTTTTTTTT CTAATTTTTA CAAAAAAAC TGCTTTAAAA
551 AAAGCTGAAA ATATTTTCTA AAACAATATT TTTGTAAAAA CTAACAAAAA
601 AATATTTTCT TCTTTTTTTC AGTTTTTAGT TAAAAATATT TAAGTTTTTT
651 CCAGTTTTTA ATTACTTTAG AAAATTACTT TTCTGCTTTT TTTTCAGTTT
701 TTACAAAAAT ATTATTTTAG AAAATATTTT TCAGTTCCTT AAAGCAGTTT
751 TTTTTTGTA AAACCTGAAA AACAATATTT TCGTTTTTTT CAGTTTTTAG
801 TAAAAATTGT TTTTAGTTTT TTTTCAGTTT TACCAAAAAT AAAATTGCTT
851 TAGAAAAATTA TTTTTCGGGT ATGGGTAATG GGTCTTTT ATTAATTAGG
901 AGATATTTTG AATTGATCAA TAGGACGATG ACACATGTCC CTCCGTTTAA
951 ATGAGGTGTA TATTTGAATC CAAAGTAAGA CTGCAGCCCG GGGGATCC

FIG. 3. (continued)

pS202-1 (SEQ ID NO:6)

1 GAATTCGATA TGGCTTGTG GACAAGAATT AATGAATCAA TTGTGAAAAA
51 GTTGATGGAC ATATTGAAGG TAAAATCATA TACTATTTTT CTAAATCTC
101 TTTTAAATGT TCCCAATTA TCTGATTTCT ATATTGCTCT TAAATGTCAC
151 TCAACCTTAG ATCAACAAAC ATATAACTTA CCCAGTACAT AAGAGATTGC
201 GGCATTATGG CTTGAAGAAA ATCCTAGAGA CACATCTGCA CCACATATTT
251 GAATTTATAC CCACAGTAAT AGAGCTCGGT TAGTACATTA TTATTATGGA
301 TGTTACGATC CGTTGCAGTA TCCATTATTA TTTTCCTTCG GTGAAAATGG
351 ATGACATTGT GGAATTAATA AAATTATTCA GACAAAAAAT TCGACGAAAC
401 GTAGAGCTTA CTGCGAACAT GAACAATTGC CCAGTATATC AAATACGTGT
451 TCAGTTGATG GATTCCTTGA TATGGAAGAT GAATCACTAC AAAGAGGAAA
501 ACGAAAAAGA GATACAGTGT CTTGTCGAGA GTATTATTGT TACAAATTC
551 AACTAAGAAA TAATGAAACA AATGAAGTGT TACATTGTGG GAGAATATTC
601 CAACAATTTA TAGTAGATAT ATATATATAA AGCTT

pS202-2 (SEQ ID NO:7)

1 AAGCTTGCAC GCCTACATCG TGGGATAATT TAGAAAAAGG AAAGGGTATA
51 TTGGATCCCC CTATCATTTG TGAAACAGGT AACCATACGA GAACCCCTTT
101 CGCTTCCTGA AAAATGTTAT ATATTGTTGT ACTCATATTT ATACACTATT
151 TATTATTAAT ATAACGATGC TTATTTTGCT TGGAGATTGG AGATTATCAC
201 AGCTTATTTA TCTTATATTG TATCTTATTA AACTTAAAAA CATAAATACT
251 ACGTGCTCTT TTAATTTGGG ATCTATTAAG GGTCGTTGC ACGCTTTTAA
301 ACATCTTGGC TATTCTGTTT ACCAGCTGCT ACCTTAGCCT GTATGCTTAC
351 ATCATCTCCT AATTTAGACA AAGGAAAGGG TATATTGGAC CCCCCTATC
401 ATTCGTGAAA CAGGTAAACA TACATTCAGA TTATACTCTT TTCAGAATGA
451 CATATTGTTT ATACATTACT GTAAATTGTG ACTATTTGTA TATTAGGGTC
501 CACATCGGGT ACATCTAACC TGCATCATGT TATCTTGAAC ACTGTTCCAA
551 TCAAAGGTTT GCACAACTT AATGTTACAA TCATGTCCAC CATACGTATG
601 CCTTGGTGCT CTTTTTTTTT CTAATGATAC TTCTTATATA TTCAGCTCAT
651 AGGCGGGCCA GAAAGGTGTG CCTGGTCACT AAAGAGCAAC GAAGTGAGTA
701 TGTTGCTCTA AAAAGGGTCC CACACTGTCA ATTCTGTCAT CCAAAGAAGT
751 TTGAATATGA ACCTCCAGGA TTTTGCTGTA ACAGTGGTTC AATAAGGTTG
801 ACATCTCATA AAATGCCAAC TGAATTATCG GAGTTATACT TTGGAAATAC
851 TGAAGAATCT GAAAATTTTC GAACTTATAT TAGAACATAC AATAACATGT
901 TTGCATTTAC TTCACCTGGT GTCAAGTATG ATAAAGAGCT AGCGAGAAGA
951 AATTGTGGTA TCTACACATT TAGAGTCCAG GGACAGATGT ATCATTTTAT
1001 AGATGATTTA GTTCCTTCCA ATGAAAAACC TAGGAATTTA TAGCTGTACT
1051 TCTACGATAA TGATAATGAA CTAGCCAAAT CAAGCTT

FIG. 3. (continued)

pS205-2 (SEQ ID NO:8)

1 GAATTCTTCA GCCATTGTAC ATATAGTTGT GTATTAATGT TATTAATAAT
51 GGATAATTAA ATATATACCT GGAATAAATA TACGATATTA TAATAGTGTG
101 TAATTATATA TAAAAATTAT ACATAATATA ATGATGGTAT TTAATATAGC
151 ATAAATTTGA ACGATCTGGA TTGATTTCTT GAATCAAAAT AGAGTTGTGT
201 GAAAAGAAAA GAATGAGATG AAAAGCAAAG TATGAAGAGA TGAATTTGTG
251 TTTTTTTTAT GGAGGAGGAA GGTTCCTCAGT GATGGAATCA TCCCTGGTTT
301 TCTTTAGCAC CAATGAAAGT AATGAACCCC CCCCCAAAAA AAAAAAAAAA
351 AAAAAAAGG GAGAGAGAGT AGAATGGAAC GGCTAGGTGA AAGTATAGGA
401 GTAGAAATTA GGTTCAAGGA GAGAAAAGGG GGGAAATTAA TTCCTAAATT
451 AATGGGATTG TAATTTTTTA ACTGTTTTGA AATATTTTAA AAGTAGTGTT
501 ATTTATATTA TTAACTTTTA AAAAAAGTCA AACGAGGTAA AAATTCCATG
551 GGGGAAAAAT TAAATGGTTA GTCTTCTATA ATATTTTCAA CTCTGCTTAG
601 CACTAAAAAT TAGTCTAAAA ATAACCCTAA ATTAGTGTAT CTAAATTAAT
651 TAGTTCATCG AACAGGAGCA TTGGATTATC CCTCCAGAGT TACACAGGAA
701 GCTT

pS206-1 (SEQ ID NO:9)

1 GGATCCAGCT ATTATTATAG CATGTGAGTT GTCCGTGAAC AGCTAATTTT
51 TTACCACACC CAAATTCAAT ACTATTTTAG TGTAATATA TCTTTTAGGT
101 CTAGTCTTAA TATTTAACTT TTTGTCTTAC TTTTAATAGA TTTTATTTGA
151 GAAAAATTAA TAATTACAAA AAATAAAAAG TATATATTCA CATACTTATA
201 GTACAAACTT TGTTTCTATT TATAAAGAGA AAAAGAAATT TTACAAAAAA
251 CAAATATATT TGCTTTCTTT TAATTAGTAG TTTTATTAAG CAAGCTATAG
301 AAGCTC

pS211-1 (SEQ ID NO:10)

1 GAATTCCTGT GTTTTAGCAC GGTGCTCAA TTGTCATATT TGGCTCATTT
51 ATCTGATTTT TAAACAATTA AGAACTTATA TGCAAATTTA ACTTTTAAAA
101 CCGCTTTTAT CATTATTTAT TTTATACAAA ATTACAACGT CGTGAAAAGG
151 CATCTCGAAC CACGCCACAA CCAGTGCACA CGTGATTTGT TGACGCATTT
201 TGGACTTCGT CAAGATCGTG ATTTGGGTGA CATAAATGTA CACCCCGTAT
251 TTAAGAAAAT AACCTTATTA AATATTGCGC CAAAATACTA CGCGTTATGA
301 TACTATTAGG GTAGGCTTGT GAATTTTACT AAATCGCCCA TCTCGGAATC
351 TAGGTATTTT CTTATATTAA AAAAAATAAG ATGGGGGCCT GCAATTTTTT
401 ATTATTTAAT ATTTATTTAT TTTTATAGCGA AGATCCCTCC CTTATTTTAT
451 GAATACCCTT TAATGACTAC ATCTTTATTA TTAATAAGTT TGTCTATAAT
501 TATGAAGTCA ATCTCTACAT ACATAAAAAAT AACATATTAA TTAATAATTT
551 AAAACAAATA TTAATGGAAA GTAATATTAC TAAAATTATA ATTACAAACA
601 ACATGGAATT GTCACAAAAT AAAAAATAAA AACTAATTAT CCCATAGTTG
651 GATTAAAATT CATATTGTGA GTATGACTTA AGCTT

FIG. 3. (continued)

pS217-1 (SEQ ID NO:11)

1 AAGCTTTAAA AGGAAGAGAG CCACAATTTT CTTTGACCTT CCTTCTCTCC
51 TAGCCACTAA GATATACAGT ACTGGTCAAA AAGAGCATAT TTATAGCTCA
101 AAATTTTGCC TTTTCTGTT GTAAACGTGA TJGTJTTCTJA CTTGGATTCT
151 TGTCTATAT ATTTACGGGA GAAAAGAGCA ATTTGCATGC TCCTAAATCT
201 TTTATTTTCT GGTGAAAAAT TGGTCTTTAA TTGGCTGGGA ATTATTTTTT
251 AGATGCTACA ACCTTGACAA ACACCTAAGA ATATTTTAGT GACAATGGCT
301 TGTCTTTGA GACTGGTTT TTCTGTTTCT GGTCCCTGTT TCAACGCCAC
351 AGCCAAAGAG TCTCGTCGTC ATTGCCCTTC GATTGGCACT CTGCAACTTA
401 AAGATTAGC ATCCAGAGAA TTTCTAGGCA AACCTTGGA TTATGCATCA
451 GATCATATTG GACTAACCA TTGGAATGTT GAACGACTTT CTGTATGTAA
501 ATCTCTGATA CATTTGCTTC TGTGTTTATA CTTGGTGTTT TCATGTTTTT
551 ATTCTTGTTT TAAATTTTTC GAGATCAAAT CATTTATAAG TATTTATTCT
601 AATGATTTTA GGCACAAGTA TCAATCGCTG CTCAGAGATG GTGGGAGAAG
651 ACCCTTAAAC CCAACATGGT AGAGATCAAT TCAGCAACAC AACTTGTTGA
701 TTCATTATTA AAAGCTGGTA ATAGATTGGT CATAATTGAC TTCTTCTCTC
751 CTAGCTGTAG AGGTTTCAAG ACTTTACATC CTAAGGTAAG ATATATAGCA
801 ATCCCCTAAA AAAAAAAAAA AAAAAAAAAA AAACCAACAA CTACATCGTA
851 ATCCTAAGCA AGTTAGGGTT AACTATATGA ATCATCACTA GACGGATCC

pS218 (SEQ ID NO:12)

1 AAGCTTAACT TTA CTACAT TGCTTTCTTT AGGGAAGCGT CTTCTTAAAT
51 GACCATCCTC TAAATTTCTC ATGAATCTTC TTCTGTTGTC CACTCTGTTA
101 TCGCTGAAAC GAAATCTGAA ATTGTCATGA TGCTGACTAT TATCCAATCA
151 CTCAGTCTCT AATTCATATT TAGATTATCT TGTTCAACAG CCCATACTGA
201 TTTTATTGTT TTTGGGGTCT AACTTTTCCT TCCGGTAGTC GGTGGAGTCT
251 ATGAACCTAT TTCTTGAAAT GAGGATATGA CTTTATGGCC TATACTCTTT
301 TGGTGTCTCA AGGCCTGTCA CCTCTCATCT TTTCTTCAA TTGACTATAG
351 ACTCTGTAAT ACTGTCATCT TTGGGATCTA CCGTTGTCCT CCATGTATCA
401 TATCTTACTC ATAATGCTTC ATTAACCTATT TTCTTATTTT CCGCTAACAT
451 TTATGTCTAT CACTTTATTC TGAAAACCTG AACAAGACAT TCTTTTCGTT
501 TTAGATCCCC TTTGCTCCAT CCAGTGGTTC TTCGGGGGAC TTAACGTTCT
551 CGCTCTCCTA GGGAGGCGAG CCACACTAAG GTAATATTTA TCCCTTCTAG
601 GCTTTCGCTG CCTATCTTCT GAGATATTTT TTTCATGCTA ATATTCACAT
651 CTAATTGTAA TTTTCTAGAG TGCGCCATCT GGGTGCCTCA CAAGAAGAGC
701 TATTAGCATC TTTGTAATAT CTTTCGGAAA TGTCAACTAA CACAACACAA
751 TCCATTACAC ATTTTGGGTT ACTCTAACCT CAGTCGGATA CTAATATCCT
801 GTCATTTTAT TAACTACAC ATGTTAGCCC CCAATAGGAT ATAACTAAGA
851 TGGGTGTGGC CAATTCTACA TACATCTGTT ACTGTTGAAA GTAAGTCGCA
901 ATGCTTTTAT TTTTCTGCCG GAGTTGAAAA TACCGATAAT CTATATTAAC
951 TGGGTACCTC GTACCCTTCT CATCTTCTCT CTTTACTTG TTGAAGCTT

FIG. 3. (continued)

pS220-1 (SEQ ID NO:13)

1 AAGCTTGAAA AAGAAGAATT AAGGCTTGCT TTCTTAATTT TTAAAAAATA
51 AAAATTATTT TGAACATCT ATACTATATT AAAAGCACGA AAACCCTATC
101 GAAATGTCGT TCGCCTTTT TACCCTTTAA AAATAATTTT ACATTAGACA
151 AAATAGTCAT TTACTATTT TTCCTAATAT ATAGGATTTT AAAATTAATT
201 TAACTTTGGC TATTAAACAT TTTCTTATAA CTTGAAATAT GTAAAACTCC
251 TAATATTTAG AAATTTAATT AACATAACCA AGGATTTTTA TATCGGTAAT
301 AACTCTAATA TGGTATCCAA ATCAGTCTAG AACTCTCTTA CCTCTAATAA
351 GTAAAAGTAC TTCTAATAAA TTCATATACT TTTTCTCTCT TCTCCGATCT
401 CTCTTTGCTC TTCTTTTAT GTATCCTTTC CTTTCTAATA GCCTTTTATG
451 AGAAGTAAAC TTTTAGGGTT GGCCCCCCT CCCCCACAA TTATATAGTT
501 TCTTACTCAG TTGTTGGAAT ATAATTCAAA TTCTTAAATA ATTGACGGTG
551 ACATTGAGTT TTA~~CTTT~~GTG GAAGAGAATT AGATTCTCGT GTTAGTAAAA
601 TCGGTTAGTA ATTGATGATG CATTATTTT ACTCTATAAT AGAGATGCAA
651 TTTTATTTT GCATTTTGGG ATCAAATTGT AATGCAGTCA TATATTGATT
701 TCATAAATGT TTGGGATATT GTTGGTTATT TAACTAGAAA TAGACTTCTT
751 ATTTCATATT TATTGTTAAA ATCCTTTATT GGAGATGAAT TATTGTTCA
801 CCGATTAGAA GTTGATAGTC GCTTTTGTT TAGAAGAAAT TTTACCGTAG
851 ACCAAGTTAA GGAGTTTTAG AAGCACTTG CATGGGAGCA TTAGTGTATG
901 TTATGGCTTT ATCAAATATA GGTTTGAAG ATTCAGAGAG CCAAGAAAAG
951 CTAGAACCCA AGAACTAGGA AGTTAGAGTA ATTCACAATA CCATAACGTG
1001 ATATAAACT TTTTATTGTA ACTCAAATCG GTAATATTTT TTGCTTTAGT
1051 CTTAATCGAT AAATTATTT TTTATATTGA TTAGTTATAG GAGGCTCACA
1101 AAGTTGGGAA TAATTA~~AAAT~~ ATCATATTT GTATTTGAAC AATTTATGAA
1151 ATAGTAATTG GTAAAAAATC ACTTTAAATT TTTATCCTAT ATCCAGAAGG
1201 ATTATGGTGT CTGGCATAGT TGT~~TT~~GGAAG ATTTGAATCA GGGTAAAAGT
1251 ATGTTGTAAT TTTTATTTTG TTATAGGCAT TTTTGTGCT TGATTGTTT
1301 GTTGTCATTA TATTTTATTA TTTGGAAGTG TATATATATG TTTGATTAAA
1351 ATATAGATAA TCAATTTTAT AAGAAATTG CAACAATTAC ACAAGGATAA
1401 AGTCTACAA ATGCGAGTAA AATTTGATTG AACCTAGGAT GTCATATTTA
1451 ATGCATATTT TATTTCAATG TGT~~TT~~ATTAT ACATCTATTG TATTATATG

FIG. 3. (continued)

CLONE	%AT	BINDING STRENGTH	GRAPHIC REPRESENTATION
pS116-1 (SEQ ID NO: 5)	76.6	90	<pre> UU U UUUUROU T T ATA TATAT T TA [] A TATTTAT AATA U OU UUUUUU </pre>
RB7-6 (SEQ ID NO: 20)	73.2	80	<pre> UORR R U UU AT AA AA A AT [] AAA O A T TA T TA U O U U </pre>
pS211-1 (SEQ ID NO: 10)	71.7	70	<pre> OR O T TATTTTAA [] A T TAAATTT O O R </pre>
pS220-1 (SEQ ID NO: 13)	73.1	70	<pre> U R URO RU A ATAAAA T TATAT TT T [] AT A A AAAAA AAT AA A R O R </pre>
pS226-1 (SEQ ID NO: 9)	77.1	60	<pre> UUO U AA A [] TATA U R U </pre>
pS205-2 (SEQ ID NO: 8)	71.4	50	<pre> R R AAA T AA T [] A TA ATT A OOUR UR </pre>
Ps217-1 (SEQ ID NO: 11)	65.2	40	<pre> OU RR AAA TT T [] AAAA AA A TT </pre>

FIG. 4.

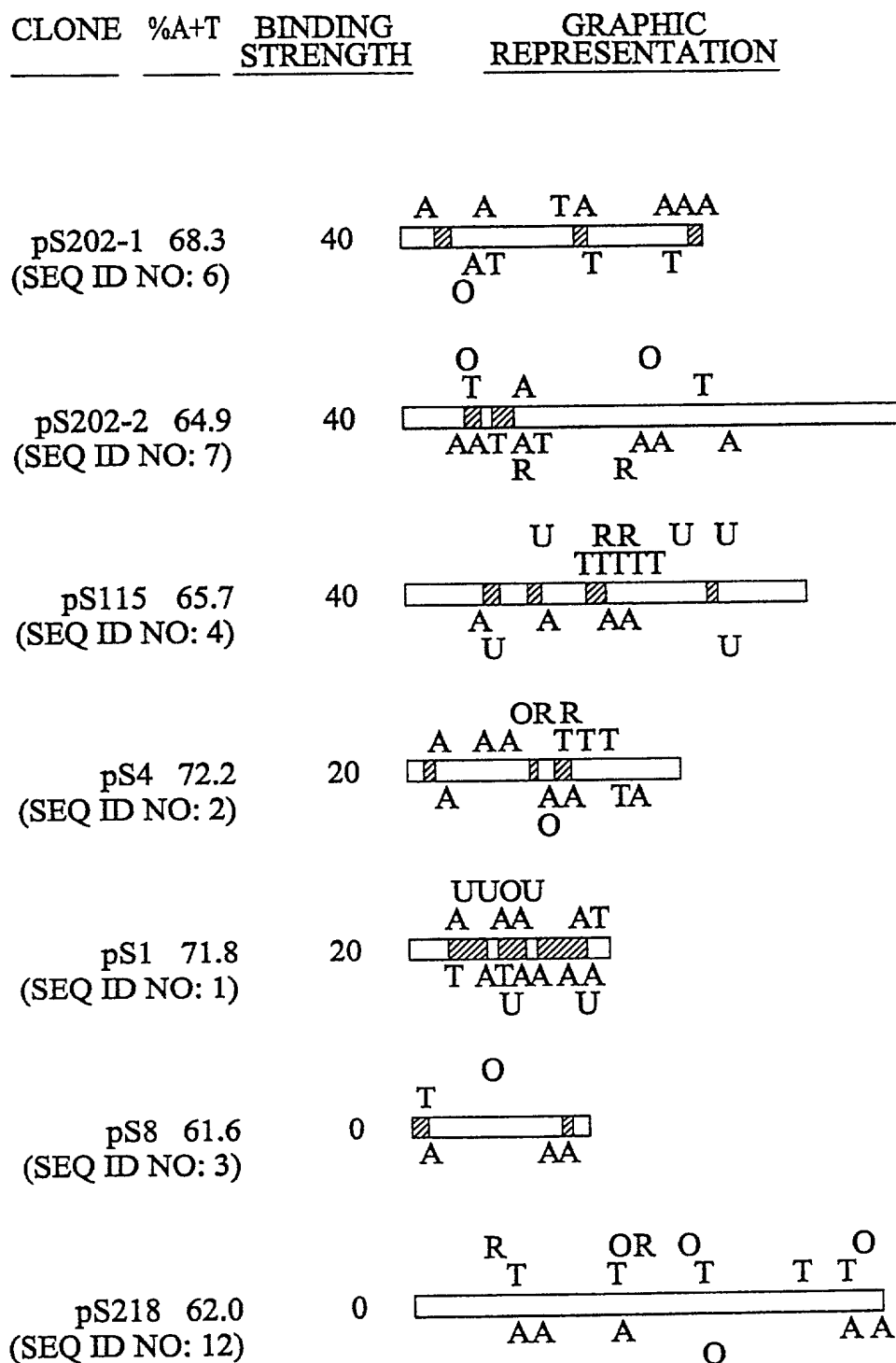


FIG. 4A.

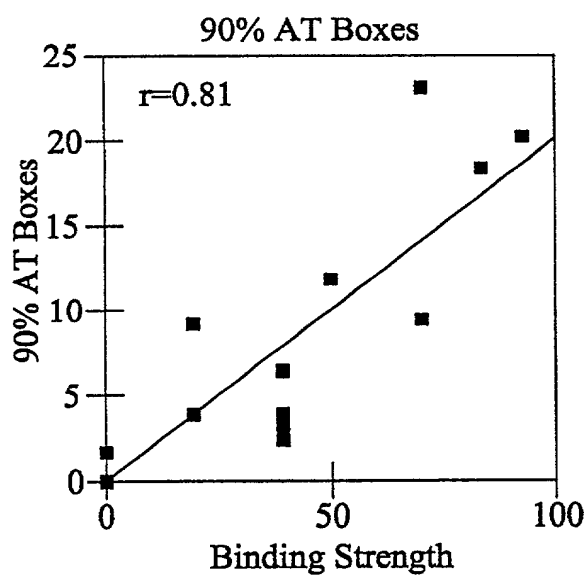


FIG. 5.

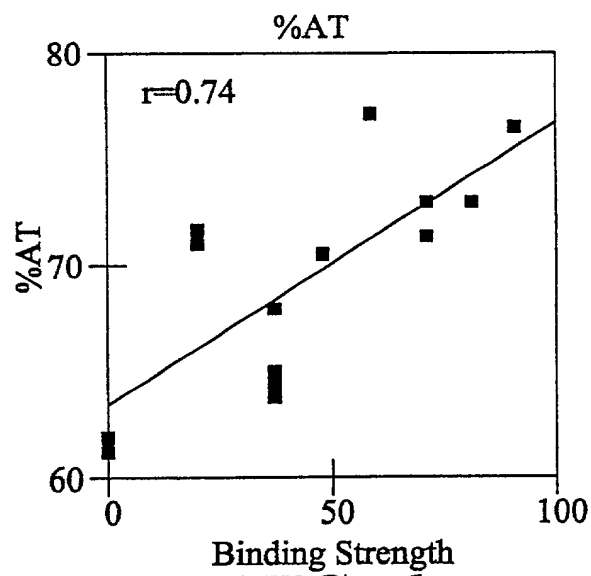


FIG. 6.

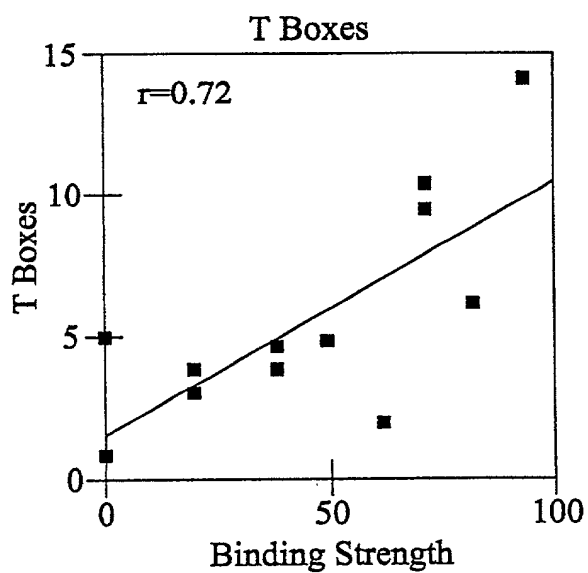


FIG. 7.

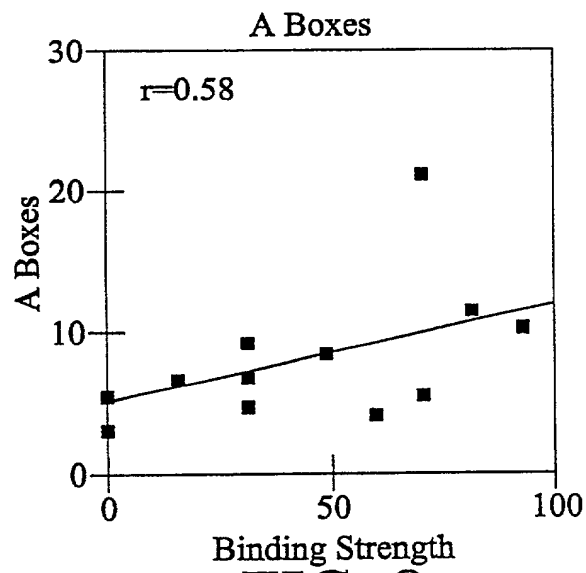


FIG. 8.

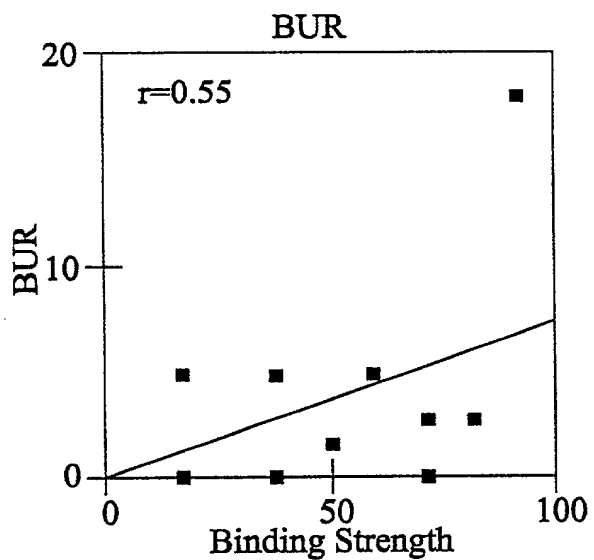


FIG. 9.

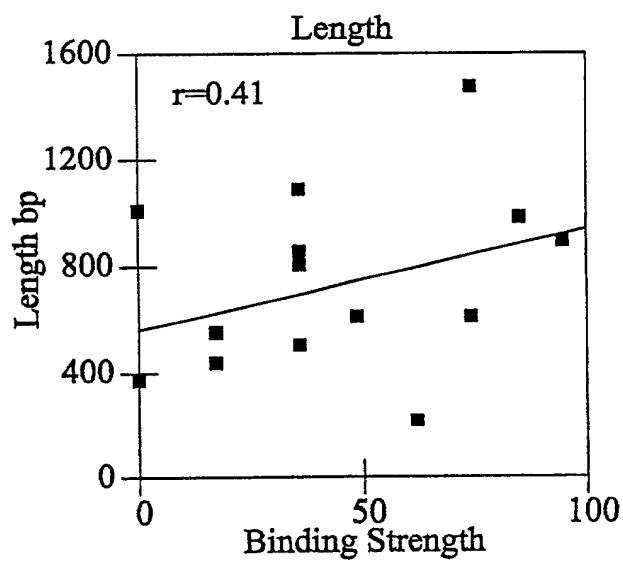


FIG. 10.

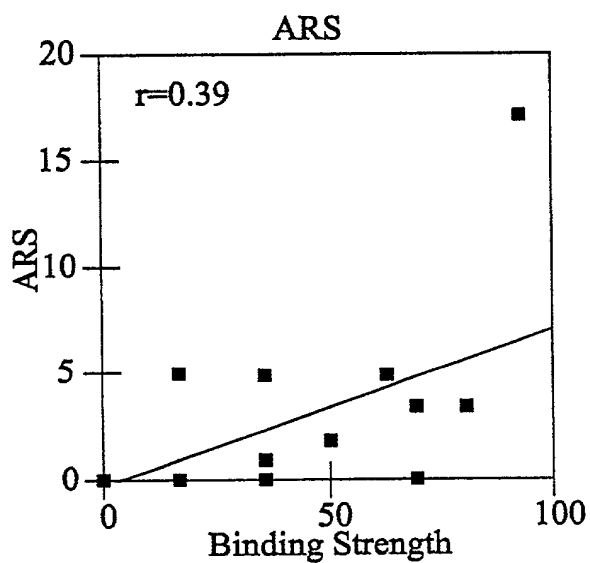


FIG. 11.

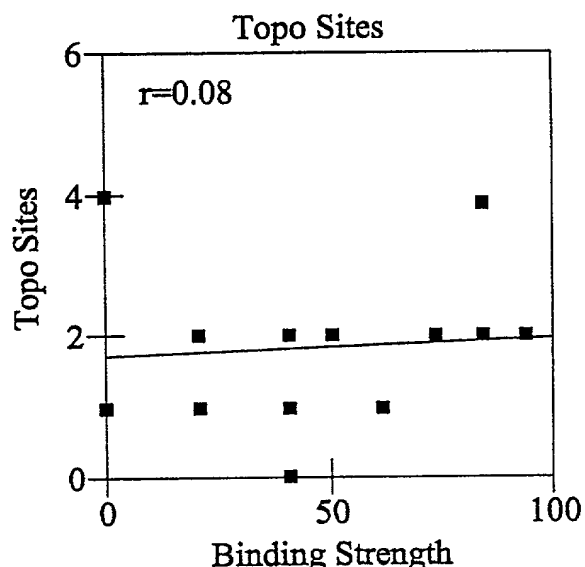


FIG. 12.